SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANTS: Waldman, Scott A.
                        Pearlman, Joshua M.
                        Barber, Michael T.
                        Schultz, Stephanie
                        Parkinson, Scott J.

    (ii) TITLE OF INVENTION: COMPOSITIONS THAT SPECIFICALLY BIND TO
                                      COLORECTAL CANCER CELLS AND METHODS OF
                                      USING THE SAME

    (iii) NUMBER OF SEQUENCES: 82

    (iv) CORRESPONDENCE ADDRESS:
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        (D) STATE: PA
        (E) COUNTRY: U.S.A.
        (F) ZIP: 19103

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: WordPerfect 6.1

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER: Not Yet Assigned
        (B) FILING DATE: Herewith
        (C) CLASSIFICATION: N/A

    (vii) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER:
        (B) FILING DATE:

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(2) INFORMATION FOR SEQ ID NO:1:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1636 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GGGCACAAGG AGTATGGTTC TAACGTGATT GGGGTCATGA AGACGTTGCT GTTGGACTTG      60

GCTTTGTGGT CACTGCTCTT CCATCCCGGG TGGCTGTCCT TTAGTTCCCA GGCCTAAATG     120

TGACTGTGAA CGCTACTTTC ATGTATTCGG ATGGTCTGAT TCATAACTCA GGCGACTGCC     180

GGAGTAGCAC CTGTGAAGGC CTCGACCTAC TCAGGAAAAT TTCAAATGCA CAACGGATGG     240

GCTGTGTCCT CATAGGGCCC TCATGTACAT ACTCCACCTT CCAGATGTAC CTTGACACAG     300

AATTGAGCTA CCCCATGATC TCAGCTGGAA GTTTTGGATT GTCATGTGAC TATAAAGAAA     360
```

```
CCTTAACCAG GCTGATGTCT CCAGCTAGAA AGTTGATATA CTTCTTGGTT AACTTTTGGA      420

AAACCAACGA TCTGCCCTTC AAAACTTATT CCTGGAGCAC TTCGTATGTT TACAAGAATG      480

GTACAGAAAC TGAGGGACTG TTTCTGGTAC CTTAATGCTC TGGAGGCTAG CGTTTCCTAT      540

TTCTCCCACG AACTCGGCTT TAAGGTGGTG TTAAGACAAG ATAAGGAGTT TCAGGATATC      600

TTAATGGACC ACAACAGGAA AAGCAATGTG ATTATTATGT GTGGTGGTCC AGAGTTCCTC      660

TACAAGCTGA AGGGTGACCG AGCAGTGGCT GAAGACATTG TCATTATTCT AGTGGATCTT      720

TTCAATGACC AGTACTTGGA GGACAATGTC ACAGCCCCTG ACTATATGAA AAATGTCCTT      780

GTTCTGACGC TGTCTCCTGG GGAATTCCCT TCTAAATAGC TCTTTCTCCA GGAATCTATC      840

ACCAACAAAA CGAGACTTTG CTCTTGCCTA TTTGAATGGA ATCCTGCTCT TTGGACATAT      900

GCTGAAGATA TTTCTTGAAA ATGGAGAAAA TATTACCACC CCCAAATTTG CTCATGCTTT      960

CAGGAATCTC ACTTTTGAAG GGTATGACGG TCCAGTGACC TTGGGATGAC TGGGGGGATG     1020

TTGACAGTAC CATGGTGCTT CCGTTATACC CTCTGTGGAC ACCAAGAAAT ACAAGGTTCT     1080

TTGGACCTAT GATACCCACG TTAATAAGAA CTATCCTGTG GATATGAGCC CCACATTCAC     1140

TTGGAAGAAC TCTAAACTTC CTAATGATAT TACAGGCCGG GGCCCTCAGA TCCTGATGAT     1200

TGCAGTCTTC ACCCTCACTG GAGCTGTGGT GCTGCTCCTG CTCGTCGCTC TCCTGATGCT     1260

CAGAAAATAT AGAAAAGATT ATGAACTTCG TCAGAAAAAA TGGTCCCACA TTCCTCCTGA     1320

AAATATCTTT CCTCTGGAGA CCAATGAGAC CAATCATGTT AGCCTCAAGA TCGATGATGA     1380

CAAAAGACGA GATACAATCC AGAGACTACG ACAGTGCAAA TACGACAAAA AGCGAGTGAT     1440

TCTCAAAGAT CTCAAGCACA ATGATGGTAA TTTCACTGAA AAACAGAAGA TAGAATTGAA     1500

CAAGTTGCTT CAGAAAGACT ATTACAACCT GACCAAGTTC TACGGCACAG TGAAACTTGA     1560

TACCATGATC TTCGGGGTGA TAGAATACTG TGAGAGAGGA TCCCCTCCGG GAAGTTTTAA     1620

ATGACACAAT TTCCTA                                                    1636
```

```
(2)  INFORMATION FOR SEQ ID NO:2:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 78 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATG AAG ACG TTG CTG TTG GAC TTG GCT TTG TGG TCA CTG CTC TTC      45
Met Lys Thr Leu Leu Leu Asp Leu Ala Leu Trp Ser Leu Leu Phe
 1               5                  10                  15

CAT CCC GGG TGG CTG TCC TTT AGT TCC CAG GCC                      78
His Pro Gly Trp Leu Ser Phe Ser Ser Gln Ala
               20                  25

(2)  INFORMATION FOR SEQ ID NO:3:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 26 amino acids
           (B) TYPE: amino acid
           (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: protein
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
```

```
Met Lys Thr Leu Leu Leu Asp Leu Ala Leu Trp Ser Leu Leu Phe
1              5               10                  15
```

```
His Pro Gly Trp Leu Ser Phe Ser Ser Gln Ala
                20                  25
```

(2) INFORMATION FOR SEQ ID NO:4:
    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 372 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
ATG TAT TCG GAT GGT CTG ATT CAT AAC TCA GGC GAC TGC CGG AGT      45
Met Tyr Ser Asp Gly Leu Ile His Asn Ser Gly Asp Cys Arg Ser
1               5               10                  15
```

```
AGC ACC TGT GAA GGC CTC GAC CTA CTC AGG AAA ATT TCA AAT GCA      90
Ser Thr Cys Glu Gly Leu Asp Leu Leu Arg Lys Ile Ser Asn Ala
                20                  25                  30
```

```
CAA CGG ATG GGC TGT GTC CTC ATA GGG CCC TCA TGT ACA TAC TCC     135
Gln Arg Met Gly Cys Val Leu Ile Gly Pro Ser Cys Thr Tyr Ser
                35                  40                  45
```

```
ACC TTC CAG ATG TAC CTT GAC ACA GAA TTG AGC TAC CCC ATG ATC     180
Thr Phe Gln Met Tyr Leu Asp Thr Glu Leu Ser Tyr Pro Met Ile
                50                  55                  60
```

```
TCA GCT GGA AGT TTT GGA TTG TCA TGT GAC TAT AAA GAA ACC TTA     225
Ser Ala Gly Ser Phe Gly Leu Ser Cys Asp Tyr Lys Glu Thr Leu
                65                  70                  75
```

```
ACC AGG CTG ATG TCT CCA GCT AGA AAG TTG ATA TAC TTC TTG GTT     270
Thr Arg Leu Met Ser Pro Ala Arg Lys Leu Ile Tyr Phe Leu Val
                80                  85                  90
```

```
AAC TTT TGG AAA ACC AAC GAT CTG CCC TTC AAA ACT TAT TCC TGG     315
Asn Phe Trp Lys Thr Asn Asp Leu Pro Phe Lys Thr Tyr Ser Trp
                95                  100                 105
```

```
AGC ACT TCG TAT GTT TAC AAG AAT GGT ACA GAA ACT GAG GGA CTG     360
Ser Thr Ser Tyr Val Tyr Lys Asn Gly Thr Glu Thr Glu Gly Leu
                110                 115                 120
```

```
TTT CTG GTA CCT                                                 372
Phe Leu Val Pro
```

(2) INFORMATION FOR SEQ ID NO:5:
    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 124 amino acids
       (B) TYPE: amino acid
       (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Met Tyr Ser Asp Gly Leu Ile His Asn Ser Gly Asp Cys Arg Ser
1               5               10                  15
```

```
Ser Thr Cys Glu Gly Leu Asp Leu Leu Arg Lys Ile Ser Asn Ala
                20                  25                  30
```

```
Gln Arg Met Gly Cys Val Leu Ile Gly Pro Ser Cys Thr Tyr Ser
                35                  40                  45
```

```
Thr Phe Gln Met Tyr Leu Asp Thr Glu Leu Ser Tyr Pro Met Ile
            50              55                      60

Ser Ala Gly Ser Phe Gly Leu Ser Cys Asp Tyr Lys Glu Thr Leu
            65              70                      75

Thr Arg Leu Met Ser Pro Ala Arg Lys Leu Ile Tyr Phe Leu Val
            80              85                      90

Asn Phe Trp Lys Thr Asn Asp Leu Pro Phe Lys Thr Tyr Ser Trp
            95              100                     105

Ser Thr Ser Tyr Val Tyr Lys Asn Gly Thr Glu Thr Glu Gly Leu
            110             115                     120

Phe Leu Val Pro
```

(2) INFORMATION FOR SEQ ID NO:6:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 276 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
ATG GGC TGT GTC CTC ATA GGG CCC TCA TGT ACA TAC TCC ACC TTC        45
Met Gly Cys Val Leu Ile Gly Pro Ser Cys Thr Tyr Ser Thr Phe
 1               5               10                      15

CAG ATG TAC CTT GAC ACA GAA TTG AGC TAC CCC ATG ATC TCA GCT        90
Gln Met Tyr Leu Asp Thr Glu Leu Ser Tyr Pro Met Ile Ser Ala
                20              25                      30

GGA AGT TTT GGA TTG TCA TGT GAC TAT AAA GAA ACC TTA ACC AGG       135
Gly Ser Phe Gly Leu Ser Cys Asp Tyr Lys Glu Thr Leu Thr Arg
                35              40                      45

CTG ATG TCT CCA GCT AGA AAG TTG ATA TAC TTC TTG GTT AAC TTT       180
Leu Met Ser Pro Ala Arg Lys Leu Ile Tyr Phe Leu Val Asn Phe
                50              55                      60

TGG AAA ACC AAC GAT CTG CCC TTC AAA ACT TAT TCC TGG AGC ACT       225
Trp Lys Thr Asn Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr
                65              70                      75

TCG TAT GTT TAC AAG AAT GGT ACA GAA ACT GAG GGA CTG TTT CTG       270
Ser Tyr Val Tyr Lys Asn Gly Thr Glu Thr Glu Gly Leu Phe Leu
                80              85                      90

GTA CCT                                                            276
Val Pro
```

(2) INFORMATION FOR SEQ ID NO:7:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 92 amino acids
           (B) TYPE: amino acid
           (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: protein
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Met Gly Cys Val Leu Ile Gly Pro Ser Cys Thr Tyr Ser Thr Phe
 1               5               10                      15

Gln Met Tyr Leu Asp Thr Glu Leu Ser Tyr Pro Met Ile Ser Ala
                20              25                      30
```

```
Gly Ser Phe Gly Leu Ser Cys Asp Tyr Lys Glu Thr Leu Thr Arg
            35                  40                  45

Leu Met Ser Pro Ala Arg Lys Leu Ile Tyr Phe Leu Val Asn Phe
            50                  55                  60

Trp Lys Thr Asn Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr
            65                  70                  75

Ser Tyr Val Tyr Lys Asn Gly Thr Glu Thr Glu Gly Leu Phe Leu
            80                  85                  90

Val Pro
```

(2) INFORMATION FOR SEQ ID NO:8:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 228 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
ATG TAC CTT GAC ACA GAA TTG AGC TAC CCC ATG ATC TCA GCT GGA      45
Met Tyr Leu Asp Thr Glu Leu Ser Tyr Pro Met Ile Ser Ala Gly
 1           5                  10                  15

AGT TTT GGA TTG TCA TGT GAC TAT AAA GAA ACC TTA ACC AGG CTG      90
Ser Phe Gly Leu Ser Cys Asp Tyr Lys Glu Thr Leu Thr Arg Leu
            20                  25                  30

ATG TCT CCA GCT AGA AAG TTG ATA TAC TTC TTG GTT AAC TTT TGG     135
Met Ser Pro Ala Arg Lys Leu Ile Tyr Phe Leu Val Asn Phe Trp
            35                  40                  45

AAA ACC AAC GAT CTG CCC TTC AAA ACT TAT TCC TGG AGC ACT TCG     180
Lys Thr Asn Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr Ser
            50                  55                  60

TAT GTT TAC AAG AAT GGT ACA GAA ACT GAG GGA CTG TTT CTG GTA     225
Tyr Val Tyr Lys Asn Gly Thr Glu Thr Glu Gly Leu Phe Leu Val
            65                  70                  75

CCT                                                            228
Pro
```

(2) INFORMATION FOR SEQ ID NO:9:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 76 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
Met Tyr Leu Asp Thr Glu Leu Ser Tyr Pro Met Ile Ser Ala Gly
 1           5                  10                  15

Ser Phe Gly Leu Ser Cys Asp Tyr Lys Glu Thr Leu Thr Arg Leu
            20                  25                  30

Met Ser Pro Ala Arg Lys Leu Ile Tyr Phe Leu Val Asn Phe Trp
            35                  40                  45

Lys Thr Asn Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr Ser
            50                  55                  60

Tyr Val Tyr Lys Asn Gly Thr Glu Thr Glu Gly Leu Phe Leu Val
```

```
          --              65                    70                    75

Pro
```

(2) INFORMATION FOR SEQ ID NO:10:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 198 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
ATG ATC TCA GCT GGA AGT TTT GGA TTG TCA TGT GAC TAT AAA GAA        45
Met Ile Ser Ala Gly Ser Phe Gly Leu Ser Cys Asp Tyr Lys Glu
 1               5                  10                  15

ACC TTA ACC AGG CTG ATG TCT CCA GCT AGA AAG TTG ATA TAC TTC        90
Thr Leu Thr Arg Leu Met Ser Pro Ala Arg Lys Leu Ile Tyr Phe
                20                  25                  30

TTG GTT AAC TTT TGG AAA ACC AAC GAT CTG CCC TTC AAA ACT TAT        135
Leu Val Asn Phe Trp Lys Thr Asn Asp Leu Pro Phe Lys Thr Tyr
                35                  40                  45

TCC TGG AGC ACT TCG TAT GTT TAC AAG AAT GGT ACA GAA ACT GAG        180
Ser Trp Ser Thr Ser Tyr Val Tyr Lys Asn Gly Thr Glu Thr Glu
                50                  55                  60

GGA CTG TTT CTG GTA CCT                                            198
Gly Leu Phe Leu Val Pro
                65
```

(2) INFORMATION FOR SEQ ID NO:11:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 66 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
Met Ile Ser Ala Gly Ser Phe Gly Leu Ser Cys Asp Tyr Lys Glu
 1               5                  10                  15

Thr Leu Thr Arg Leu Met Ser Pro Ala Arg Lys Leu Ile Tyr Phe
                20                  25                  30

Leu Val Asn Phe Trp Lys Thr Asn Asp Leu Pro Phe Lys Thr Tyr
                35                  40                  45

Ser Trp Ser Thr Ser Tyr Val Tyr Lys Asn Gly Thr Glu Thr Glu
                50                  55                  60

Gly Leu Phe Leu Val Pro
                65
```

(2) INFORMATION FOR SEQ ID NO:12:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 138 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
ATG TCT CCA GCT AGA AAG TTG ATA TAC TTC TTG GTT AAC TTT TGG        45
```

```
Met Ser Pro Ala Arg Lys Leu Ile Tyr Phe Leu Val Asn Phe Trp
  1           5               10                    15
```

```
AAA ACC AAC GAT CTG CCC TTC AAA ACT TAT TCC TGG AGC ACT TCG        90
Lys Thr Asn Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr Ser
              20              25                    30
```

```
TAT GTT TAC AAG AAT GGT ACA GAA ACT GAG GGA CTG TTT CTG GTA       135
Tyr Val Tyr Lys Asn Gly Thr Glu Thr Glu Gly Leu Phe Leu Val
              35              40                    45
```

```
CCT                                                               138
Pro
```

(2) INFORMATION FOR SEQ ID NO:13:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 46 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
Met Ser Pro Ala Arg Lys Leu Ile Tyr Phe Leu Val Asn Phe Trp
  1           5               10                    15
```

```
Lys Thr Asn Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr Ser
              20              25                    30
```

```
Tyr Val Tyr Lys Asn Gly Thr Glu Thr Glu Gly Leu Phe Leu Val
              35              40                    45
```

```
Pro
```

(2) INFORMATION FOR SEQ ID NO:14:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 27 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
ATG CAC AAC GGA TGG GCT GTG TCC TCA                                27
Met His Asn Gly Trp Ala Val Ser Ser
  1           5
```

(2) INFORMATION FOR SEQ ID NO:15:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 9 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
Met His Asn Gly Trp Ala Val Ser Ser
  1           5
```

(2) INFORMATION FOR SEQ ID NO:16:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
ATG TAC ATA CTC CAC CTT CCA GAT GTA CCT                            30
```

```
Met Tyr Ile Leu His Leu Pro Asp Val Pro
1               5               10
```

(2) INFORMATION FOR SEQ ID NO:17:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 10 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: protein
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
Met Tyr Ile Leu His Leu Pro Asp Val Pro
1               5               10
```

(2) INFORMATION FOR SEQ ID NO:18:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 351 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
ATG TTT ACA AGA ATG GTA CAG AAA CTG AGG GAC TGT TTC TGG TAC     45
Met Phe Thr Arg Met Val Gln Lys Leu Arg Asp Cys Phe Trp Tyr
1               5               10              15

CTT AAT GCT CTG GAG GCT AGC GTT TCC TAT TTC TCC CAC GAA CTC     90
Leu Asn Ala Leu Glu Ala Ser Val Ser Tyr Phe Ser His Glu Leu
                20              25              30

GGC TTT AAG GTG GTG TTA AGA CAA GAT AAG GAG TTT CAG GAT ATC     135
Gly Phe Lys Val Val Leu Arg Gln Asp Lys Glu Phe Gln Asp Ile
                35              40              45

TTA ATG GAC CAC AAC AGG AAA AGC AAT GTG ATT ATT ATG TGT GGT     180
Leu Met Asp His Asn Arg Lys Ser Asn Val Ile Ile Met Cys Gly
                50              55              60

GGT CCA GAG TTC CTC TAC AAG CTG AAG GGT GAC CGA GCA GTG GCT     225
Gly Pro Glu Phe Leu Tyr Lys Leu Lys Gly Asp Arg Ala Val Ala
                65              70              75

GAA GAC ATT GTC ATT ATT CTA GTG GAT CTT TTC AAT GAC CAG TAC     270
Glu Asp Ile Val Ile Ile Leu Val Asp Leu Phe Asn Asp Gln Tyr
                80              85              90

TTG GAG GAC AAT GTC ACA GCC CCT GAC TAT ATG AAA AAT GTC CTT     315
Leu Glu Asp Asn Val Thr Ala Pro Asp Tyr Met Lys Asn Val Leu
                95              100             105

GTT CTG ACG CTG TCT CCT GGG GAA TTC CCT TCT AAA                 351
Val Leu Thr Leu Ser Pro Gly Glu Phe Pro Ser Lys
                110             115
```

(2) INFORMATION FOR SEQ ID NO:19:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 117 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: protein
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
Met Phe Thr Arg Met Val Gln Lys Leu Arg Asp Cys Phe Trp Tyr
1               5               10              15

Leu Asn Ala Leu Glu Ala Ser Val Ser Tyr Phe Ser His Glu Leu
                20              25              30
```

```
Gly Phe Lys Val Val Leu Arg Gln Asp Lys Glu Phe Gln Asp Ile
        35                    40                    45

Leu Met Asp His Asn Arg Lys Ser Asn Val Ile Ile Met Cys Gly
        50                    55                    60

Gly Pro Glu Phe Leu Tyr Lys Leu Lys Gly Asp Arg Ala Val Ala
        65                    70                    75

Glu Asp Ile Val Ile Ile Leu Val Asp Leu Phe Asn Asp Gln Tyr
        80                    85                    90

Leu Glu Asp Asn Val Thr Ala Pro Asp Tyr Met Lys Asn Val Leu
        95                    100                   105

Val Leu Thr Leu Ser Pro Gly Glu Phe Pro Ser Lys
        110                   115
```

(2) INFORMATION FOR SEQ ID NO:20:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 339 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
ATG GTA CAG AAA CTG AGG GAC TGT TTC TGG TAC CTT AAT GCT CTG      45
Met Val Gln Lys Leu Arg Asp Cys Phe Trp Tyr Leu Asn Ala Leu
 1                5                   10                  15

GAG GCT AGC GTT TCC TAT TTC TCC CAC GAA CTC GGC TTT AAG GTG      90
Glu Ala Ser Val Ser Tyr Phe Ser His Glu Leu Gly Phe Lys Val
                 20                  25                  30

GTG TTA AGA CAA GAT AAG GAG TTT CAG GAT ATC TTA ATG GAC CAC     135
Val Leu Arg Gln Asp Lys Glu Phe Gln Asp Ile Leu Met Asp His
                 35                  40                  45

AAC AGG AAA AGC AAT GTG ATT ATT ATG TGT GGT GGT CCA GAG TTC     180
Asn Arg Lys Ser Asn Val Ile Ile Met Cys Gly Gly Pro Glu Phe
                 50                  55                  60

CTC TAC AAG CTG AAG GGT GAC CGA GCA GTG GCT GAA GAC ATT GTC     225
Leu Tyr Lys Leu Lys Gly Asp Arg Ala Val Ala Glu Asp Ile Val
                 65                  70                  75

ATT ATT CTA GTG GAT CTT TTC AAT GAC CAG TAC TTG GAG GAC AAT     270
Ile Ile Leu Val Asp Leu Phe Asn Asp Gln Tyr Leu Glu Asp Asn
                 80                  85                  90

GTC ACA GCC CCT GAC TAT ATG AAA AAT GTC CTT GTT CTG ACG CTG     315
Val Thr Ala Pro Asp Tyr Met Lys Asn Val Leu Val Leu Thr Leu
                 95                  100                 105

TCT CCT GGG GAA TTC CCT TCT AAA                                 339
Ser Pro Gly Glu Phe Pro Ser Lys
                 110
```

(2) INFORMATION FOR SEQ ID NO:21:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
Met Val Gln Lys Leu Arg Asp Cys Phe Trp Tyr Leu Asn Ala Leu
 1           5               10              15

Glu Ala Ser Val Ser Tyr Phe Ser His Glu Leu Gly Phe Lys Val
            20              25              30

Val Leu Arg Gln Asp Lys Glu Phe Gln Asp Ile Leu Met Asp His
                35          40              45

Asn Arg Lys Ser Asn Val Ile Ile Met Cys Gly Gly Pro Glu Phe
                50              55              60

Leu Tyr Lys Leu Lys Gly Asp Arg Ala Val Ala Glu Asp Ile Val
                65          70              75

Ile Ile Leu Val Asp Leu Phe Asn Asp Gln Tyr Leu Glu Asp Asn
                80          85              90

Val Thr Ala Pro Asp Tyr Met Lys Asn Val Leu Val Leu Thr Leu
                95          100             105

Ser Pro Gly Glu Phe Pro Ser Lys
                110
```

(2) INFORMATION FOR SEQ ID NO:22:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 213 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
ATG GAC CAC AAC AGG AAA AGC AAT GTG ATT ATT ATG TGT GGT GGT     45
Met Asp His Asn Arg Lys Ser Asn Val Ile Ile Met Cys Gly Gly
 1           5               10              15

CCA GAG TTC CTC TAC AAG CTG AAG GGT GAC CGA GCA GTG GCT GAA     90
Pro Glu Phe Leu Tyr Lys Leu Lys Gly Asp Arg Ala Val Ala Glu
            20              25              30

GAC ATT GTC ATT ATT CTA GTG GAT CTT TTC AAT GAC CAG TAC TTG     135
Asp Ile Val Ile Ile Leu Val Asp Leu Phe Asn Asp Gln Tyr Leu
                35          40              45

GAG GAC AAT GTC ACA GCC CCT GAC TAT ATG AAA AAT GTC CTT GTT     180
Glu Asp Asn Val Thr Ala Pro Asp Tyr Met Lys Asn Val Leu Val
                50          55              60

CTG ACG CTG TCT CCT GGG GAA TTC CCT TCT AAA                     213
Leu Thr Leu Ser Pro Gly Glu Phe Pro Ser Lys
                65          70
```

(2) INFORMATION FOR SEQ ID NO:23:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 71 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
Met Asp His Asn Arg Lys Ser Asn Val Ile Ile Met Cys Gly Gly
 1           5               10              15

Pro Glu Phe Leu Tyr Lys Leu Lys Gly Asp Arg Ala Val Ala Glu
            20              25              30
```

```
Asp Ile Val Ile Ile Leu Val Asp Leu Phe Asn Asp Gln Tyr Leu
              35              40              45

Glu Asp Asn Val Thr Ala Pro Asp Tyr Met Lys Asn Val Leu Val
              50              55              60

Leu Thr Leu Ser Pro Gly Glu Phe Pro Ser Lys
              65              70
```

(2) INFORMATION FOR SEQ ID NO:24:
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 180 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
ATG TGT GGT GGT CCA GAG TTC CTC TAC AAG CTG AAG GGT GAC CGA    45
Met Cys Gly Gly Pro Glu Phe Leu Tyr Lys Leu Lys Gly Asp Arg
1               5               10              15

GCA GTG GCT GAA GAC ATT GTC ATT ATT CTA GTG GAT CTT TTC AAT    90
Ala Val Ala Glu Asp Ile Val Ile Ile Leu Val Asp Leu Phe Asn
                20              25              30

GAC CAG TAC TTG GAG GAC AAT GTC ACA GCC CCT GAC TAT ATG AAA    135
Asp Gln Tyr Leu Glu Asp Asn Val Thr Ala Pro Asp Tyr Met Lys
                35              40              45

AAT GTC CTT GTT CTG ACG CTG TCT CCT GGG GAA TTC CCT TCT AAA    180
Asn Val Leu Val Leu Thr Leu Ser Pro Gly Glu Phe Pro Ser Lys
                50              55              60
```

(2) INFORMATION FOR SEQ ID NO:25:
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 60 amino acids
         (B) TYPE: amino acid
         (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: protein
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
Met Cys Gly Gly Pro Glu Phe Leu Tyr Lys Leu Lys Gly Asp Arg
1               5               10              15

Ala Val Ala Glu Asp Ile Val Ile Ile Leu Val Asp Leu Phe Asn
                20              25              30

Asp Gln Tyr Leu Glu Asp Asn Val Thr Ala Pro Asp Tyr Met Lys
                35              40              45

Asn Val Leu Val Leu Thr Leu Ser Pro Gly Glu Phe Pro Ser Lys
                50              55              60
```

(2) INFORMATION FOR SEQ ID NO:26:
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 51 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```
ATG AAA AAT GTC CTT GTT CTG ACG CTG TCT CCT GGG GAA TTC CCT    45
Met Lys Asn Val Leu Val Leu Thr Leu Ser Pro Gly Glu Phe Pro
1               5               10              15

TCT AAA                                                        51
Ser Lys
```

(2) INFORMATION FOR SEQ ID NO:27:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
Met Lys Asn Val Leu Val Leu Thr Leu Ser Pro Gly Glu Phe Pro
 1           5               10                  15

Ser Lys
```

(2) INFORMATION FOR SEQ ID NO:28:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 57 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```
ATG CTC TGG AGG CTA GCG TTT CCT ATT TCT CCC ACG AAC TCG GCT    45
Met Leu Trp Arg Leu Ala Phe Pro Ile Ser Pro Thr Asn Ser Ala
 1           5               10                  15

TTA AGG TGG TGT                                                57
Leu Arg Trp Cys
```

(2) INFORMATION FOR SEQ ID NO:29:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 19 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```
Met Leu Trp Arg Leu Ala Phe Pro Ile Ser Pro Thr Asn Ser Ala
 1           5               10                  15

Leu Arg Trp Cys
```

(2) INFORMATION FOR SEQ ID NO:30:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 42 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```
ATG ACC AGT ACT TGG AGG ACA ATG TCA CAG CCC CTG ACT ATA    42
Met Thr Ser Thr Trp Arg Thr Met Ser Gln Pro Leu Thr Ile
 1           5               10
```

(2) INFORMATION FOR SEQ ID NO:31:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 14 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```
Met Thr Ser Thr Trp Arg Thr Met Ser Gln Pro Leu Thr Ile
 1           5               10
```

(2) INFORMATION FOR SEQ ID NO:32:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```
ATG TCA CAG CCC CTG ACT ATA                                    21
Met Ser Gln Pro Leu Thr Ile
 1               5
```

(2) INFORMATION FOR SEQ ID NO:33:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 7 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```
Met Ser Gln Pro Leu Thr Ile
 1               5
```

(2) INFORMATION FOR SEQ ID NO:34:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 27 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```
ATG GAA TCC TGC TCT TTG GAC ATA TGC                            27
Met Glu Ser Cys Ser Leu Asp Ile Cys
 1               5
```

(2) INFORMATION FOR SEQ ID NO:35:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 9 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```
Met Glu Ser Cys Ser Leu Asp Ile Cys
 1               5
```

(2) INFORMATION FOR SEQ ID NO:36:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 108 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```
ATG CTG AAG ATA TTT CTT GAA AAT GGA GAA AAT ATT ACC ACC CCC    45
Met Leu Lys Ile Phe Leu Glu Asn Gly Glu Asn Ile Thr Thr Pro
 1               5                  10                  15

AAA TTT GCT CAT GCT TTC AGG AAT CTC ACT TTT GAA GGG TAT GAC    90
Lys Phe Ala His Ala Phe Arg Asn Leu Thr Phe Glu Gly Tyr Asp
                20                  25                  30

GGT CCA GTG ACC TTG GGA                                        108
Gly Pro Val Thr Leu Gly
                35
```

(2) INFORMATION FOR SEQ ID NO:37:

```
          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 36 amino acids
               (B) TYPE: amino acid
               (D) TOPOLOGY: linear
          (ii) MOLECULE TYPE: protein
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:


ATG CTG AAG ATA TTT CTT GAA AAT GGA GAA AAT ATT ACC ACC CCC        45
Met Leu Lys Ile Phe Leu Glu Asn Gly Glu Asn Ile Thr Thr Pro
 1               5                  10                  15


AAA TTT GCT CAT GCT TTC AGG AAT CTC ACT TTT GAA GGG TAT GAC        90
Lys Phe Ala His Ala Phe Arg Asn Leu Thr Phe Glu Gly Tyr Asp
                    20                  25                  30


GGT CCA GTG ACC TTG GGA                                            108
Gly Pro Val Thr Leu Gly
                35


(2) INFORMATION FOR SEQ ID NO:38:
         (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 75 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:


ATG GAG AAA ATA TTA CCA CCC CCA AAT TTG CTC ATG CTT TCA GGA        45
Met Glu Lys Ile Leu Pro Pro Pro Asn Leu Leu Met Leu Ser Gly
 1               5                  10                  15


ATC TCA CTT TTG AAG GGT ATG ACG GTC CAG                            75
Ile Ser Leu Leu Lys Gly Met Thr Val Gln
                20                  25


(2) INFORMATION FOR SEQ ID NO:39:
         (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 25 amino acids
               (B) TYPE: amino acid
               (D) TOPOLOGY: linear
         (ii) MOLECULE TYPE: protein
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:


Met Glu Lys Ile Leu Pro Pro Pro Asn Leu Leu Met Leu Ser Gly
 1               5                  10                  15


Ile Ser Leu Leu Lys Gly Met Thr Val Gln
                20                  25


(2) INFORMATION FOR SEQ ID NO:40:
         (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 42 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:


ATG CTT TCA GGA ATC TCA CTT TTG AAG GGT ATG ACG GTC CAG            42
Met Leu Ser Gly Ile Ser Leu Leu Lys Gly Met Thr Val Gln
 1               5                  10


(2) INFORMATION FOR SEQ ID NO:41:
         (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 14 amino acids
               (B) TYPE: amino acid
               (D) TOPOLOGY: linear
         (ii) MOLECULE TYPE: protein
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```
Met Leu Ser Gly Ile Ser Leu Leu Lys Gly Met Thr Val Gln
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:42:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 84 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```
ATG ACT GGG GGG ATG TTG ACA GTA CCA TGG TGC TTC CGT TAT ACC    45
Met Thr Gly Gly Met Leu Thr Val Pro Trp Cys Phe Arg Tyr Thr
1               5                   10                  15

CTC TGT GGA CAC CAA GAA ATA CAA GGT TCT TTG GAC CTA            84
Leu Cys Gly His Gln Glu Ile Gln Gly Ser Leu Asp Leu
                20                  25
```

(2) INFORMATION FOR SEQ ID NO:43:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 28 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```
Met Thr Gly Gly Met Leu Thr Val Pro Trp Cys Phe Arg Tyr Thr
1               5                   10                  15

Leu Cys Gly His Gln Glu Ile Gln Gly Ser Leu Asp Leu
                20                  25
```

(2) INFORMATION FOR SEQ ID NO:44:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 72 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```
ATG TTG ACA GTA CCA TGG TGC TTC CGT TAT ACC CTC TGT GGA CAC    45
Met Leu Thr Val Pro Trp Cys Phe Arg Tyr Thr Leu Cys Gly His
1               5                   10                  15

CAA GAA ATA CAA GGT TCT TTG GAC CTA                            72
Gln Glu Ile Gln Gly Ser Leu Asp Leu
                20
```

(2) INFORMATION FOR SEQ ID NO:45:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```
Met Leu Thr Val Pro Trp Cys Phe Arg Tyr Thr Leu Cys Gly His
1               5                   10                  15

Gln Glu Ile Gln Gly Ser Leu Asp Leu
                20
```

(2) INFORMATION FOR SEQ ID NO:46:
    (i) SEQUENCE CHARACTERISTICS:

```
         (A) LENGTH: 93 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:
```

```
ATG GTG CTT CCG TTA TAC CCT CTG TGG ACA CCA AGA AAT ACA AGG     45
Met Val Leu Pro Leu Tyr Pro Leu Trp Thr Pro Arg Asn Thr Arg
1            5                 10                    15
```

```
TTC TTT GGA CCT ATG ATA CCC ACG TTA ATA AGA ACT ATC CTG TGG     90
Phe Phe Gly Pro Met Ile Pro Thr Leu Ile Arg Thr Ile Leu Trp
              20              25                    30
```

```
ATA                                                             93
Ile
```

```
(2) INFORMATION FOR SEQ ID NO:47:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 31 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:
```

```
Met Val Leu Pro Leu Tyr Pro Leu Trp Thr Pro Arg Asn Thr Arg
1            5                 10                    15
```

```
Phe Phe Gly Pro Met Ile Pro Thr Leu Ile Arg Thr Ile Leu Trp
              20              25                    30
```

```
Ile
```

```
(2) INFORMATION FOR SEQ ID NO:48:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 36 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:
```

```
ATG ATA CCC ACG TTA ATA AGA ACT ATC CTG TGG ATA              36
Met Ile Pro Thr Leu Ile Arg Thr Ile Leu Trp Ile
1            5                 10
```

```
(2) INFORMATION FOR SEQ ID NO:49:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 12 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:
```

```
Met Ile Pro Thr Leu Ile Arg Thr Ile Leu Trp Ile
1            5                 10
```

```
(2) INFORMATION FOR SEQ ID NO:50:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 498 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:
```

```
ATG AGC CCC ACA TTC ACT TGG AAG AAC TCT AAA CTT CCT AAT GAT     45
Met Ser Pro Thr Phe Thr Trp Lys Asn Ser Lys Leu Pro Asn Asp
```

```
     1       --         5                    10                         15
   ATT ACA GGC CGG GGC CCT CAG ATC CTG ATG ATT GCA GTC TTC ACC        90
   Ile Thr Gly Arg Gly Pro Gln Ile Leu Met Ile Ala Val Phe Thr
               20                      25                      30

   CTC ACT GGA GCT GTG GTG CTG CTC CTG CTC GTC GCT CTC CTG ATG       135
   Leu Thr Gly Ala Val Val Leu Leu Leu Leu Val Ala Leu Leu Met
               35                      40                      45

   CTC AGA AAA TAT AGA AAA GAT TAT GAA CTT CGT CAG AAA AAA TGG       180
   Leu Arg Lys Tyr Arg Lys Asp Tyr Glu Leu Arg Gln Lys Lys Trp
               50                      55                      60

   TCC CAC ATT CCT CCT GAA AAT ATC TTT CCT CTG GAG ACC AAT GAG       225
   Ser His Ile Pro Pro Glu Asn Ile Phe Pro Leu Glu Thr Asn Glu
               65                      70                      75

   ACC AAT CAT GTT AGC CTC AAG ATC GAT GAT GAC AAA AGA CGA GAT       270
   Thr Asn His Val Ser Leu Lys Ile Asp Asp Asp Lys Arg Arg Asp
               80                      85                      90

   ACA ATC CAG AGA CTA CGA CAG TGC AAA TAC GAC AAA AAG CGA GTG       315
   Thr Ile Gln Arg Leu Arg Gln Cys Lys Tyr Asp Lys Lys Arg Val
               95                     100                     105

   ATT CTC AAA GAT CTC AAG CAC AAT GAT GGT AAT TTC ACT GAA AAA       360
   Ile Leu Lys Asp Leu Lys His Asn Asp Gly Asn Phe Thr Glu Lys
               110                     115                     120

   CAG AAG ATA GAA TTG AAC AAG TTG CTT CAG AAA GAC TAT TAC AAC       405
   Gln Lys Ile Glu Leu Asn Lys Leu Leu Gln Lys Asp Tyr Tyr Asn
               125                     130                     135

   CTG ACC AAG TTC TAC GGC ACA GTG AAA CTT GAT ACC ATG ATC TTC       450
   Leu Thr Lys Phe Tyr Gly Thr Val Lys Leu Asp Thr Met Ile Phe
               140                     145                     150

   GGG GTG ATA GAA TAC TGT GAG AGA GGA TCC CCT CCG GGA AGT TTT       495
   Gly Val Ile Glu Tyr Cys Glu Arg Gly Ser Pro Pro Gly Ser Phe
               155                     160                     165

   AAA                                                              498
   Lys
```

(2) INFORMATION FOR SEQ ID NO:51:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 166 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```
Met Ser Pro Thr Phe Thr Trp Lys Asn Ser Lys Leu Pro Asn Asp
 1               5                   10                      15

Ile Thr Gly Arg Gly Pro Gln Ile Leu Met Ile Ala Val Phe Thr
                20                      25                      30

Leu Thr Gly Ala Val Val Leu Leu Leu Leu Val Ala Leu Leu Met
                35                      40                      45

Leu Arg Lys Tyr Arg Lys Asp Tyr Glu Leu Arg Gln Lys Lys Trp
                50                      55                      60

Ser His Ile Pro Pro Glu Asn Ile Phe Pro Leu Glu Thr Asn Glu
```

```
                    65                      70                      75
Thr Asn His Val Ser Leu Lys Ile Asp Asp Asp Lys Arg Arg Asp
                80                      85                      90
Thr Ile Gln Arg Leu Arg Gln Cys Lys Tyr Asp Lys Lys Arg Val
                95                     100                     105
Ile Leu Lys Asp Leu Lys His Asn Asp Gly Asn Phe Thr Glu Lys
               110                     115                     120
Gln Lys Ile Glu Leu Asn Lys Leu Leu Gln Lys Asp Tyr Tyr Asn
               125                     130                     135
Leu Thr Lys Phe Tyr Gly Thr Val Lys Leu Asp Thr Met Ile Phe
               140                     145                     150
Gly Val Ile Glu Tyr Cys Glu Arg Gly Ser Pro Pro Gly Ser Phe
               155                     160                     165

Lys
```

(2) INFORMATION FOR SEQ ID NO:52:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 426 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```
ATG ATT GCA GTC TTC ACC CTC ACT GGA GCT GTG GTG CTG CTC CTG     45
Met Ile Ala Val Phe Thr Leu Thr Gly Ala Val Val Leu Leu Leu
 1               5                  10                      15

CTC GTC GCT CTC CTG ATG CTC AGA AAA TAT AGA AAA GAT TAT GAA     90
Leu Val Ala Leu Leu Met Leu Arg Lys Tyr Arg Lys Asp Tyr Glu
               20                  25                      30

CTT CGT CAG AAA AAA TGG TCC CAC ATT CCT CCT GAA AAT ATC TTT    135
Leu Arg Gln Lys Lys Trp Ser His Ile Pro Pro Glu Asn Ile Phe
               35                  40                      45

CCT CTG GAG ACC AAT GAG ACC AAT CAT GTT AGC CTC AAG ATC GAT    180
Pro Leu Glu Thr Asn Glu Thr Asn His Val Ser Leu Lys Ile Asp
               50                  55                      60

GAT GAC AAA AGA CGA GAT ACA ATC CAG AGA CTA CGA CAG TGC AAA    225
Asp Asp Lys Arg Arg Asp Thr Ile Gln Arg Leu Arg Gln Cys Lys
               65                  70                      75

TAC GAC AAA AAG CGA GTG ATT CTC AAA GAT CTC AAG CAC AAT GAT    270
Tyr Asp Lys Lys Arg Val Ile Leu Lys Asp Leu Lys His Asn Asp
               80                  85                      90

GGT AAT TTC ACT GAA AAA CAG AAG ATA GAA TTG AAC AAG TTG CTT    315
Gly Asn Phe Thr Glu Lys Gln Lys Ile Glu Leu Asn Lys Leu Leu
               95                 100                     105

CAG AAA GAC TAT TAC AAC CTG ACC AAG TTC TAC GGC ACA GTG AAA    360
Gln Lys Asp Tyr Tyr Asn Leu Thr Lys Phe Tyr Gly Thr Val Lys
              110                 115                     120

CTT GAT ACC ATG ATC TTC GGG GTG ATA GAA TAC TGT GAG AGA GGA    405
Leu Asp Thr Met Ile Phe Gly Val Ile Glu Tyr Cys Glu Arg Gly
              125                 130                     135
```

```
TCC CCT CCG GGA AGT TTT AAA                                    426
Ser Pro Pro Gly Ser Phe Lys
                140
```

(2) INFORMATION FOR SEQ ID NO:53:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 142 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: protein
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```
Met Ile Ala Val Phe Thr Leu Thr Gly Ala Val Val Leu Leu Leu
1               5                  10                  15

Leu Val Ala Leu Leu Met Leu Arg Lys Tyr Arg Lys Asp Tyr Glu
                20                  25                  30

Leu Arg Gln Lys Lys Trp Ser His Ile Pro Pro Glu Asn Ile Phe
                35                  40                  45

Pro Leu Glu Thr Asn Glu Thr Asn His Val Ser Leu Lys Ile Asp
                50                  55                  60

Asp Asp Lys Arg Arg Asp Thr Ile Gln Arg Leu Arg Gln Cys Lys
                65                  70                  75

Tyr Asp Lys Lys Arg Val Ile Leu Lys Asp Leu Lys His Asn Asp
                80                  85                  90

Gly Asn Phe Thr Glu Lys Gln Lys Ile Glu Leu Asn Lys Leu Leu
                95                  100                 105

Gln Lys Asp Tyr Tyr Asn Leu Thr Lys Phe Tyr Gly Thr Val Lys
                110                 115                 120

Leu Asp Thr Met Ile Phe Gly Val Ile Glu Tyr Cys Glu Arg Gly
                125                 130                 135

Ser Pro Pro Gly Ser Phe Lys
                140
```

(2) INFORMATION FOR SEQ ID NO:54:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 366 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```
ATG CTC AGA AAA TAT AGA AAA GAT TAT GAA CTT CGT CAG AAA AAA    45
Met Leu Arg Lys Tyr Arg Lys Asp Tyr Glu Leu Arg Gln Lys Lys
1               5                  10                  15

TGG TCC CAC ATT CCT CCT GAA AAT ATC TTT CCT CTG GAG ACC AAT    90
Trp Ser His Ile Pro Pro Glu Asn Ile Phe Pro Leu Glu Thr Asn
                20                  25                  30

GAG ACC AAT CAT GTT AGC CTC AAG ATC GAT GAT GAC AAA AGA CGA    135
Glu Thr Asn His Val Ser Leu Lys Ile Asp Asp Asp Lys Arg Arg
                35                  40                  45

GAT ACA ATC CAG AGA CTA CGA CAG TGC AAA TAC GAC AAA AAG CGA    180
Asp Thr Ile Gln Arg Leu Arg Gln Cys Lys Tyr Asp Lys Lys Arg
                50                  55                  60

GTG ATT CTC AAA GAT CTC AAG CAC AAT GAT GGT AAT TTC ACT GAA    225
```

Val Ile Leu Lys Asp Leu Lys His Asn Asp Gly Asn Phe Thr Glu
            65   70   75

AAA CAG AAG ATA GAA TTG AAC AAG TTG CTT CAG AAA GAC TAT TAC   270
Lys Gln Lys Ile Glu Leu Asn Lys Leu Leu Gln Lys Asp Tyr Tyr
            80   85   90

AAC CTG ACC AAG TTC TAC GGC ACA GTG AAA CTT GAT ACC ATG ATC   315
Asn Leu Thr Lys Phe Tyr Gly Thr Val Lys Leu Asp Thr Met Ile
            95   100   105

TTC GGG GTG ATA GAA TAC TGT GAG AGA GGA TCC CCT CCG GGA AGT   360
Phe Gly Val Ile Glu Tyr Cys Glu Arg Gly Ser Pro Pro Gly Ser
            110   115   120

TTT AAA   366
Phe Lys

(2) INFORMATION FOR SEQ ID NO:55:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 122 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met Leu Arg Lys Tyr Arg Lys Asp Tyr Glu Leu Arg Gln Lys Lys
 1   5   10   15

Trp Ser His Ile Pro Pro Glu Asn Ile Phe Pro Leu Glu Thr Asn
            20   25   30

Glu Thr Asn His Val Ser Leu Lys Ile Asp Asp Asp Lys Arg Arg
            35   40   45

Asp Thr Ile Gln Arg Leu Arg Gln Cys Lys Tyr Asp Lys Lys Arg
            50   55   60

Val Ile Leu Lys Asp Leu Lys His Asn Asp Gly Asn Phe Thr Glu
            65   70   75

Lys Gln Lys Ile Glu Leu Asn Lys Leu Leu Gln Lys Asp Tyr Tyr
            80   85   90

Asn Leu Thr Lys Phe Tyr Gly Thr Val Lys Leu Asp Thr Met Ile
            95   100   105

Phe Gly Val Ile Glu Tyr Cys Glu Arg Gly Ser Pro Pro Gly Ser
            110   115   120

Phe Lys

(2) INFORMATION FOR SEQ ID NO:56:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 57 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

ATG ATC TTC GGG GTG ATA GAA TAC TGT GAG AGA GGA TCC CCT CCG   45
Met Ile Phe Gly Val Ile Glu Tyr Cys Glu Arg Gly Ser Pro Pro
 1   5   10   15

GGA AGT TTT AAA   57

Gly Ser Phe Lys

(2) INFORMATION FOR SEQ ID NO:57:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 19 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```
Met Ile Phe Gly Val Ile Glu Tyr Cys Glu Arg Gly Ser Pro Pro
1               5               10              15
```

Gly Ser Phe Lys

(2) INFORMATION FOR SEQ ID NO:58:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```
ATG ATA TTA CAG GCC GGG GCC CTC AGA TCC                30
Met Ile Leu Gln Ala Gly Ala Leu Arg Ser
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:59:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```
Met Ile Leu Gln Ala Gly Ala Leu Arg Ser
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:60:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 156 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```
ATG AAC TTC GTC AGA AAA AAT GGT CCC ACA TTC CTC CTG AAA ATA    45
Met Asn Phe Val Arg Lys Asn Gly Pro Thr Phe Leu Leu Lys Ile
1               5                   10                  15

TCT TTC CTC TGG AGA CCA ATG AGA CCA ATC ATG TTA GCC TCA AGA    90
Ser Phe Leu Trp Arg Pro Met Arg Pro Ile Met Leu Ala Ser Arg
                20                  25                  30

TCG ATG ATG ACA AAA GAC GAG ATA CAA TCC AGA GAC TAC GAC AGT    135
Ser Met Met Thr Lys Asp Glu Ile Gln Ser Arg Asp Tyr Asp Ser
                35                  40                  45

GCA AAT ACG ACA AAA AGC GAG                                    156
Ala Asn Thr Thr Lys Ser Glu
                50
```

(2) INFORMATION FOR SEQ ID NO:61:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 52 amino acids

```
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: protein
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:
```

```
Met Asn Phe Val Arg Lys Asn Gly Pro Thr Phe Leu Leu Lys Ile
1               5               10              15
```

```
Ser Phe Leu Trp Arg Pro Met Arg Pro Ile Met Leu Ala Ser Arg
                20              25              30
```

```
Ser Met Met Thr Lys Asp Glu Ile Gln Ser Arg Asp Tyr Asp Ser
                35              40              45
```

```
Ala Asn Thr Thr Lys Ser Glu
                50
```

```
(2) INFORMATION FOR SEQ ID NO:62:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 93 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:
```

```
ATG AGA CCA ATC ATG TTA GCC TCA AGA TCG ATG ATG ACA AAA GAC      45
Met Arg Pro Ile Met Leu Ala Ser Arg Ser Met Met Thr Lys Asp
1               5               10              15
```

```
GAG ATA CAA TCC AGA GAC TAC GAC AGT GCA AAT ACG ACA AAA AGC      90
Glu Ile Gln Ser Arg Asp Tyr Asp Ser Ala Asn Thr Thr Lys Ser
                20              25              30
```

```
GAG                                                              93
Glu
```

```
(2) INFORMATION FOR SEQ ID NO:63:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 31 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: protein
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:
```

```
Met Arg Pro Ile Met Leu Ala Ser Arg Ser Met Met Thr Lys Asp
1               5               10              15
```

```
Glu Ile Gln Ser Arg Asp Tyr Asp Ser Ala Asn Thr Thr Lys Ser
                20              25              30
```

```
Glu
```

```
(2) INFORMATION FOR SEQ ID NO:64:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 81 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:
```

```
ATG TTA GCC TCA AGA TCG ATG ATG ACA AAA GAC GAG ATA CAA TCC      45
Met Leu Ala Ser Arg Ser Met Met Thr Lys Asp Glu Ile Gln Ser
1               5               10              15
```

```
AGA GAC TAC GAC AGT GCA AAT ACG ACA AAA AGC GAG                  81
```

Arg Asp Tyr Asp Ser Ala Asn Thr Thr Lys Ser Glu
            20   25

(2) INFORMATION FOR SEQ ID NO:65:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 27 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: protein
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Leu Ala Ser Arg Ser Met Met Thr Lys Asp Glu Ile Gln Ser
 1   5   10   15

Arg Asp Tyr Asp Ser Ala Asn Thr Thr Lys Ser Glu
            20   25

(2) INFORMATION FOR SEQ ID NO:66:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 63 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ATG ATG ACA AAA GAC GAG ATA CAA TCC AGA GAC TAC GAC AGT GCA   45
Met Met Thr Lys Asp Glu Ile Gln Ser Arg Asp Tyr Asp Ser Ala
 1   5   10   15

AAT ACG ACA AAA AGC GAG   63
Asn Thr Thr Lys Ser Glu
            20

(2) INFORMATION FOR SEQ ID NO:67:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 21 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: protein
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met Met Thr Lys Asp Glu Ile Gln Ser Arg Asp Tyr Asp Ser Ala
 1   5   10   15

Asn Thr Thr Lys Ser Glu
            20

(2) INFORMATION FOR SEQ ID NO:68:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 60 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ATG ACA AAA GAC GAG ATA CAA TCC AGA GAC TAC GAC AGT GCA AAT   45
Met Thr Lys Asp Glu Ile Gln Ser Arg Asp Tyr Asp Ser Ala Asn
 1   5   10   15

ACG ACA AAA AGC GAG   60
Thr Thr Lys Ser Glu
            20

(2) INFORMATION FOR SEQ ID NO:69:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20 amino acids
          (B) TYPE: amino acid

```
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Thr Lys Asp Glu Ile Gln Ser Arg Asp Tyr Asp Ser Ala Asn
1               5                   10                  15

Thr Thr Lys Ser Glu
                 20

(2) INFORMATION FOR SEQ ID NO:70:
    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 18 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATG GTC CCA CAT TCC TCC                                    18
Met Val Pro His Ser Ser
1               5

(2) INFORMATION FOR SEQ ID NO:71:
    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 6 amino acids
         (B) TYPE: amino acid
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Val Pro His Ser Ser
1               5

(2) INFORMATION FOR SEQ ID NO:72:
    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 30 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

ATG ATG GTA ATT TCA CTG AAA AAC AGA AGA                   30
Met Met Val Ile Ser Leu Lys Asn Arg Arg
1               5                   10

(2) INFORMATION FOR SEQ ID NO:73:
    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 10 amino acids
         (B) TYPE: amino acid
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Met Met Val Ile Ser Leu Lys Asn Arg Arg
1               5                   10

(2) INFORMATION FOR SEQ ID NO:74:
    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 27 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

ATG GTA ATT TCA CTG AAA AAC AGA AGA                       27
Met Val Ile Ser Leu Lys Asn Arg Arg
1               5
```

(2) INFORMATION FOR SEQ ID NO:75:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 9 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
   (ii) MOLECULE TYPE: protein
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Met Val Ile Ser Leu Lys Asn Arg Arg
 1   5

(2) INFORMATION FOR SEQ ID NO:76:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 42 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ATG GCG GCC GGG AGC ATG CGA CGT CGG CCC ATT CGC CCT ATA   42
Met Ala Ala Gly Ser Met Arg Arg Arg Pro Ile Arg Pro Ile
 1   5   10

(2) INFORMATION FOR SEQ ID NO:77:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 14 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
   (ii) MOLECULE TYPE: protein
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met Ala Ala Gly Ser Met Arg Arg Arg Pro Ile Arg Pro Ile
 1   5   10

(2) INFORMATION FOR SEQ ID NO:78:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 27 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ATG CGA CGT CGG CCC ATT CGC CCT ATA   27
Met Arg Arg Arg Pro Ile Arg Pro Ile
 1   5

(2) INFORMATION FOR SEQ ID NO:79:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 9 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
   (ii) MOLECULE TYPE: protein
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Arg Arg Arg Pro Ile Arg Pro Ile
 1   5

(2) INFORMATION FOR SEQ ID NO:80:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 15 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ATG ACA CAA TTT CCT   15
Met Thr Gln Phe Pro

1   --   5

(2) INFORMATION FOR SEQ ID NO:81:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 5 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Met Thr Gln Phe Pro
 1   5

(2) INFORMATION FOR SEQ ID NO:82:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH:
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: unknown
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```
TGGAGTGGGCTGAGGGACTCCACTAGAGGCTGTCCATCTGGATTCCCTGCCTCCCTAGGAGCCCAACAGAGCAAAGCAAG 80
TGGGCACAAGGAGTATGGTTCTAACGTGATTGGGGTGATGAAGACGTTGCTGTTGGACTTGGCTTTGTGGTCACTGCTCT
TCCAGCCCGGGTGGCTGTCCTTTAGTTCCCAGC
                                                GCCTAAATGTGACTGTGAACCCTACTTTCATGTATTCGGATGGTCTGATTCATAACTCAGGCGACT
GCCGGAGTAGCACCTGTGAAGGCCTCGACCTACTCAGGAAAATTTCAAATGCACAACGGATGGGCTGTGTCCTCATAGGG
CCCTCATGTACATACTCCACCTTCCAGATGTACCTTGACACAGAATTGAGCTACCCCATGATCTCAGCTGGAAGTTTTGG
ATTGTCATGTGACTATAAAGAAACCTTAACCAGGCTGATGTCTCCAGCTAGAAAGTTGATGTACTTCTTGGTTAACTTTT
GGAAAACCAACGATCTGCCCTTCAAAACTTATTCCTGGAGCACTTCGTATGTTTACAAGAATGGTACAGAAACTGAGGAC
TGTTTCTGGTACCTTAATGCTCTGGAGGCTAGCGTTTCCTATTTCTCCCACGAACTCGGCTTTAAGGTGGTGTTAAGACA
AGATAAGGAGTTTCAGGATATCTTAATGGACCACAACAGGAAAAGCAATGTGATTATTATGTGTGGTGGTCCAGAGTTCC
TCTACAAGCTGAAGGGTGACCGAGCAGTGGCTGAAGACATTGTCATTATTCTAGTGGATCTTTTCAATGACCAGTACTTG
GAGGACAATGTCACAGCCCCTGACTATATGAAAAATGTCCTTGTTCTGACGCTGTCTCCTGGGAATTCCCTTCTAAATAG
CTCTTTCTCCAGGAATCTATCACCAACAAAACGACACTTTCGTCTTGCCTATTTGAATGGAATCCTCGTCTTTGGACATA
TGCTGAAGATATTTCTTGAAAATGGAGAAAATATTACCACCCCAAATTTGCTCATGCCTTCAGGAATCTCACTTTTGAA
GGGTATGACGGTCCAGTGACCTTGGATGACTCGGGGGGATGTTGACAGTACCATGGTGCTTCTGTATACCTCTGTGGACAC
CAAGAAATACAAGGTTCTTTTGACCTATGATACCCACGTAAATAAGACCTATCCTGTGGATATGAGCCCCACATTCACTT
CGAAGAACTCTAAACTTCCTAATGATATTACAGGCCGGGGCCCTCAGATCCTGATGATTGCAGTCTTCACCCTCACTGGA
GCTGTGGTGCTGCTCCTGCTCGTCGCTCTCCTGATGCTCAGAAAATATAGAAAAGATTATGAACTTCGTCAGAAAAATG
GTCCCACATTCCTCCTGAAAATATCTTTCCTCTGGAGACCAATGAGACCAATCATGTTAGCCTCAAGATCGATGATGACA
AAAGACGAGATACAATCCAGAGACTACGACAGTGCAAATACGTCAAAAAGCGAGTGATTCTCAAAGATCTCAAGCACAAT
GATGGTAATTTCACTGAAAAACAGAAGATAGAATTGAACAAGTTGCTTCAGATTGACTATTACACCCTAACCAAGTTCTA
CGGGACAGTCAAACTGGATACCATGATCTTTCGGGGTGATAGAATACTGTGAGAGAGGATCCTCCGGGAAGTTTTAAATG
ACACAATTTCCTACCCTGATGGCACATTCATGGATTGGGAGTTTAAGATCTCTGTCTTGTATGACATTGCTAAGGGAATG
TCATATCTGCACTCCAGTAAGACAGAAGTCCATGGTCGTCTGAAATCTACCAACTGCGTAGTGGACAGTAGAATGGTGGT
GAAGATCACTGATTTTGGCTGCAATTCCATTTTGCCTCCAAAAAAGGACCTGTGGACAGCTCCAGAGCACCTCCGCCAAG
CCAACATCTCTCAGAAAGGAGATGTGTACAGCTATGGGATCATCGCACAGGAGATCATTCTGCGGAAAGAAACCTTCTAC
ACTTTGAGCTGTCGGGACCGGAATGAGAAGATTTTCAGAGTGGAAAAATTCCAATGGAATGAAACCCTTCCGCCCAGATTT
ATTCTTGGAAACAGCAGAGGAAAAAGAGCCTAGAAGTGTACCTACTTGTAAAAAACTGTTGGGAGGAAGATCCAGAAAAGA
GACCAGATTTCAAAAAAATTGAGACTACACTTGCCAAGATATTTGGACTTTTTCATGACCAAAAAAATGAAAGCTATATG
GATACCTTGATCCGACGTCTACAGCTATATTCTCGAAACCTGGAACATCTGGTAGAGGAAAGGACACAGCTGTACAAGGC
AGAGAGGGACAGGGCTGACAGACTTAACTTTATGTTGCTTCCAAGGCTAGTGGTAAAGTCTCTGAAGGAGAAAGGCTTTG
TGGAGCCGGAACTATATGAGGAAGTTACAATCTACTTCAGTGACATTGTAGGTTTCACTACTATCTGCAAATACAGCACC
CCCATGGAAGTGGTGGACATGCTTAATGACATCTATAAGAGTTTTGACCACATTGTTGATCATCATGATGTCTACAAGGT
GGAAACCATCGGTGATGCGTACATGGTGGCTAGTGGTTTGCCTAAGAGAAATGGCAATCGGCATGCAATAGACATTGCCA
AGATGGCCTTGGAAATCCTCAGCTTCATGGGGACCTTTGAGCTGGAGCATCTTCCTGGCCTCCCAATATGGATTCGCATT
GGAGTTCACTCTGGTCCCTGTGCTGCTGGAGTTGTGGGAATCAAGATGCCTCGTTATTGTCTATTGGAGATACGGTCAA
CACAGCCTCTAGGATGGAATCCACTGGCCTCCCTTTGAGAATTCACGTGAGTGGCTCCACCATAGCCATCCTGAAGAGAA
CTGAGTGCCAGTTCCTTTATGAAGTGAGAGGAGAAACATACTTAAAGGGGAAGAGGAAAGAGACTACCTACTGGCTGACT
GGGATGAAGGACCAGAAATTCAACCTGCCAACCCCTCCTACTGTGGAGAATCAACAGCGTTTGCAAGCAGAATTTTCAGA
CATGATTGCCAACTCTTTACAGAAAAGACAGGCAGCAGGGATAAGAAGCCAAAAACCCAGACGGGTAGCCAGCTATAAAA
AAGGCACTCTGGAATACTTGCAGCTGAATACCACAGACAAGGAGAGCACCTATTTTTAAACCTAAATGAGGTATAAGGAC
TCACACAAATTAAAATACAGCTGCACTGAGGCCAGGCACCCTCAGGTGTCCTGAAAGCTTACTTTCCTGAGACCTCATGA
GGCAGAAATGTCTTAGGCTTGGCTGCCCTGTTTGGACCATGGACTTTCTTTGCATGAATCAGATGTGTTTCTCAGTGAAAT
AACTACCTTCCACTCTGGAACCTTATTCCAGCAGTTGTTCCAGGGAGCTTCTACCTGGAAAAGAAAAGAATTTCATTTAT
TTTTTGTTTGTTTATTTTTATCGTTTTTGTTTACTGGCTTTCCTTCTGTATTCATAAGATTTTTTAAATTGTCATAATTA
TATTTTAAATACCCATCTTCATTAAAGTATATTTAACTCATAATTTTTGCAGAAAATATGCTATATATTAGGCAAGAATA
AAAGCTAAAGGTTTCCCAAAAAAAAAA
```